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<p>(54) Title: DETECTION OF RETROVIRAL SUBTYPES BASED UPON ENVELOPE SPECIFIC SEQUENCES</p>			
<p>(57) Abstract</p> <p>The present invention is based upon the finding that porcine endogenous retroviruses exist in two different subtypes, which we have termed PERV-A and PERV-B. The differences are reflected in sequence divergence in the envelope genes, and these differences may be used to provide nucleic acid and antibody probes which can distinguish between the two subtypes. This allows patterns of subtype transmission between cells, particularly porcine to human cells, to be monitored.</p>			

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DETECTION OF RETROVIRAL SUBTYPES BASED UPON
ENVELOPE SPECIFIC SEQUENCES

The present invention relates to methods and products for the detection of porcine endogenous retroviruses.

There is currently much interest in the development of xenotransplantation of organs to meet the shortage of human organs available for transplant. Considerable progress has been made in developing transgenic animals, particularly pigs, whose organs have been modified to remove immunogenic surface antigens and/or to present human antigen, or to inhibit components of the human immune system. However while progress has been made on the immunological problems of xenotransplantation, relatively little research has been conducted on the risk of infection being transmitted to an organ recipient by the presence of endogenous pathogens in the donor organ.

Recently, Patience et al, *Nature Medicine*, 1997, 3;282-286, reported the results of a study of pig endogenous retroviruses (PERVs) in porcine cell lines. The authors demonstrated that two different pig kidney cell lines, PK15 and MPK, produced endogenous retroviruses and the PK15 retroviruses were capable of infecting a human cell line (kidney 293 cells). Analysis of the protease and reverse transcriptase genes of the retroviruses infecting these cell lines showed that there was about 95% sequence similarity at the amino acid level between isolates from the two cell lines. This information was used to design nucleic acid primers for the analysis of DNA from porcine tissue and the authors demonstrated that multiple PERV related sequences existed in such tissue and were expressed. The primers were specific for porcine PERVs and did not detect sequences in human or murine cells.

WO97/21836, published on 19 June 1997, describes three porcine retrovirus isolates. These isolates are currently described as PERV-A and PERV-C, with SEQ ID NO:1 and SEQ ID NO:3 of

WO97/21836 being of the PERV-C type, and SEQ ID NO:2 being of the PERV-A type.

WO97/40167, published on 30 October 1997, describes a retrovirus isolate from the PK-15 porcine cell line. This isolate is currently described in the art as being of a PERV-B type. Figure 3 of WO97/40167 sets out a sequence with 3 open reading frames indicated to be the *gag*, *pol* and *env* genes of the retrovirus. Figure 1 of WO97/40167 sets out a shorter sequence with a 3' end which extends into the 5' region of the *env* gene. There are differences between the 3' end of Figure 1 and the corresponding region of Figure 3. The differences are attributed in WO97/40167 to improvements in carrying out and analysing the sequence obtained.

Disclosure of the invention.

Prior to the present invention, it had not been appreciated that PERVs existed in different subtypes. Prior to the publication of WO97/21836 and WO97/40167 we surprisingly identified two subtypes of this virus, which we designated PERV-A and PERV-B. More surprisingly, although the majority of individual isolates from the PK15 cell line are PERV-A isolates (29/32 tested), our initial data indicated that human 293 cells infected with the virus are exclusively or almost exclusively of the PERV-B subtype. Thus although the primers used by Patience et al are capable of detecting numerous PERV sequences in porcine tissue and cell lines, these primers do not distinguish between the two subtypes of PERV.

In the light of the present invention we believe that the sequence of Figure 1 of WO97/40167 is derived from a PERV-A isolate, since the Figure 1 sequence in the region of difference is substantially similar to the corresponding portion of the PERV-A isolate described herein.

In a first aspect the present invention thus provides an

isolated nucleic acid probe, said probe being capable of hybridising to the PERV-B env gene under conditions in which said probe is substantially unable to hybridise to the PERV-A env gene. This is referred to below as a PERV-B specific probe (or "primer" or "oligonucleotide"). The terms "probe", "primer" and "oligonucleotide" are used synonymously.

In a second aspect, the invention provides an isolated nucleic acid probe, said probe being capable of hybridising to the PERV-A env gene under conditions in which said probe is substantially unable to hybridise to the PERV-B env gene. This is referred to below as a PERV-A specific probe (or "primer" or "oligonucleotide").

Although the env gene sequences are shown as the positive strand, it is to be understood that probes of the invention may be directed to either strand where integrated or cDNA retroviral sequences are to be detected. Where retroviral RNA is to be detected, a probe capable of hybridising to the positive strand is required (in the case of PCR initially to make cDNA).

In a further aspect, the invention provides a pair of primers suitable for conducting a polymerase chain reaction, at least one of said primers being a nucleic acid as defined above specific for the PERV-A or PERV-B genes. The probes and primers of the invention may be used in a method of detecting retroviruses in a sample of porcine or human tissue. Such tissue includes primary porcine tissue and human cell lines which have been cultivated in the presence of a porcine cell line, or human tissues which are from a human patient who has received a xenotransplant. Nucleic acid (e.g. mRNA, total RNA, DNA or total nucleic acid) from the tissues or cells may be probed directly or if desired retroviral sequences may be amplified using primers suitable for amplifying retroviral sequences in general (e.g. LTR primers) prior to detecting PERV env sequences of the invention, thus allowing those of

skill in the art to distinguish between the PERV-A and PERV-B subtypes. The nucleic acid may be present in a sample comprising human or porcine tissue or cells, or may be cloned nucleic acid from such sources.

5 The differences between the two genes is reflected by changes to the env proteins, and these differences are believed to include differences to antigenic determinants (referred to herein as epitopes) in the two subtypes of proteins, which thus allows the development of antibodies which are capable of 10 binding to an epitope on the PERV-B env protein under conditions where they are substantially unable to bind to the PERV-A env protein, and vice versa. These antibodies may be used in a method of detecting the presence of a pig endogenous 15 retrovirus in porcine or human tissue or cell lines, thus allowing those of skill in the art to distinguish between the PERV-A and PERV-B subtypes.

Detailed Description of the Invention.

Our prototype isolate of the PERV-A env gene region is shown in SEQ ID NO. 1, and the envelope polypeptide encoded by 20 nucleotides 211 to 2190 of SEQ ID NO. 1 is shown as SEQ ID NO. 2. For the purposes of the present invention, the PERV-A env gene is at least 80%, preferably at least 90% and more 25 preferably at least 95% homologous to the coding sequence of SEQ ID NO. 1. Homologous sequences include those which encode the same polypeptide shown in SEQ ID NO:2 but differ from SEQ ID NO:1 due to the degeneracy of the genetic code.

The percentage homology (also referred to as identity) of DNA sequences can be calculated using commercially available 30 algorithms, such as Lasergene software from DNASTAR Inc or the algorithm GAP (Genetics Computer Group, Madison, WI). GAP uses the Needleman and Wunsch algorithm to align two complete sequences that maximizes the number of matches and minimizes the number of gaps. Generally, the default parameters are

used, with a gap creation penalty = 12 and gap extension penalty = 4. Use of either of the terms "homology" and "homologous" herein does not imply any necessary evolutionary relationship between compared sequences, in keeping for example with standard use of terms such as "homologous recombination" which merely requires that two nucleotide sequences are sufficiently similar to recombine under the appropriate conditions.

10 Similarly, our prototype isolate of the PERV-B env gene region is shown in SEQ ID NO. 3, and the envelope polypeptide encoded by nucleotides 911 to 2881 of SEQ ID NO. 3 is shown as SEQ ID NO. 4. For the purposes of the present invention, the PERV-B env gene is at least 80%, preferably at least 90% and more preferably at least 95% homologous to the coding sequence of 15 SEQ ID NO. 3. Homologous sequences include those which encode the same polypeptide shown in SEQ ID NO:4 but differ from SEQ ID NO:3 due to the degeneracy of the genetic code.

20 An alignment of SEQ ID NO. 1 and SEQ ID NO. 3 is shown as Figure 1.

25 The PERV-B specific probe of the invention is preferably derived from the 5' end of the env gene of PERV-B, particularly from the region of PERV-B corresponding to nucleotides 1000 to 2500 of the SEQ ID NO. 3 isolate. More preferably the region corresponds to nucleotides 1100 to 1900.

30 It is to be understood that "derived" means conceptually derived, and physical isolation of the nucleic acid from the gene (as opposed to, for example, de novo synthesis) is not necessary.

35 Specific PERV-B probes include oligonucleotides consisting of a contiguous sequence of from 10 to 40 nucleotides of a PERV-B isolate derived from the sequence of SEQ ID NO:3 from 1000 to 2500, preferably 1100 to 1900, or the complement thereof.

Such oligonucleotides include SEQ ID NO:7 (1376-1395 of SEQ ID NO:3) and SEQ ID NO:8 (complement of 1620-1639 of SEQ ID NO:3) shown in Example 3 below comprise 8 and 14 differences respectively in their sequences and the corresponding regions of SEQ ID NO:1 as follows:

5 PERV-B 5' TTCTCCTTGTCAA--TTCCGG 3' (SEQ ID NO:7)
* * * * * *

PERV-A 5' TACTCTTTGTTAACAAATCCTA 3' (SEQ ID NO:9)

and:

10 PERV-B 5' TACTTTATCGGGTCCCACTG 3' (SEQ ID NO:8)
* * * * * *****

PERV-A 5' TATTCTGAGGCGCGAATAGT 3' (SEQ ID NO:10)

Similarly, the PERV-A specific probe of the invention may be derived from the regions shown in Figure 1 which correspond to the abovementioned preferred and most preferred regions of PERV-A. Thus PERV-A specific probes include oligonucleotides consisting of a contiguous sequence of from 10 to 40 nucleotides of a PERV-A isolate derived from the sequence of SEQ ID NO:1 from 300 to 1809, preferably 400 to 1209, or the complement thereof.

20 Thus for example such oligonucleotides include SEQ ID NO:5 (742-760 of SEQ ID NO:1) and SEQ ID NO:6 (complement of 1082-1101 of SEQ ID NO:1) shown in Example 3 below. These comprise 10 and 21 differences respectively in their sequences and the corresponding regions of SEQ ID NO:3.

25 By "differences", it is meant substitutions, deletions and insertions. As can be seen from Figure 1, the primers of SEQ ID NOS:5-8 include between them all these differences from the corresponding portions of the reference isolate.

30 The above-mentioned probes may additionally include, at their

3' and/or 5' termini, linker sequences (typically of from 3 to 8 nucleotides) of non-PERV-B or -A sequence. Linker sequences include those containing a restriction enzyme recognition sequence allowing the oligonucleotides to be introduced into or excised from a cloning or expression vector.

Nucleic acid probes of the invention may be obtained by first of all comparing the PERV-A and PERV-B sequences of Figure 1 (or of other PERV-A and PERV-B isolates) and regions of the sequences which are sufficiently different to provide specific probes determined. This may be done by any suitable means, for example by calculating the predicted T_m of a probe when annealed to a specific region of the PERV-A or PERV-B sequences using a suitable algorithm or empirically by experiment. When by experiment this can be achieved by blotting the PERV-A and PERV-B sequences onto a nitrocellulose filter and probing the filter with a labelled putative probe under hybridising conditions. Probes of the invention will be able to hybridise to the PERV sequence of choice and not to the other PERV sequence under those conditions. Thus a PERV-B specific probe of the invention will be capable of hybridising to the sequence of SEQ ID NO:3 under conditions in which the probe does not hybridise to SEQ ID NO:1. Similarly, a PERV-A specific probe of the invention will be capable of hybridising to the sequence of SEQ ID NO:1 under conditions in which it does not hybridise to SEQ ID NO:3.

Hybridisation conditions will be selected to be commensurate with the size of the probe and can be determined by reference to standard text books such as Sambrook et al, Molecular Cloning, 1989, Cold Spring Harbour.

It will be understood by those of skill in the art that hybridisation conditions will vary depending upon whether a probe of the invention is hybridised to nucleic acid fixed to a solid support or is hybridised to a target nucleic acid in a liquid phase. In the case of the former (eg Southern or

Northern blotting) a probe of the invention will be annealed under low stringency conditions and subsequently washed under high stringency conditions such that the probe will remain annealed to its target PERV sequence and not to the corresponding sequence of the other subtype. Where a probe of the invention is for use as a PCR primer annealing conditions will be selected in accordance with standard protocols such that the probe will hybridise to its target subtype nucleic acid and not to non-target subtype nucleic acid. Thus it will be understood that reference to hybridisation of a probe to target nucleic acid includes hybridisation achieved by blotting and washing on a solid phase as well as annealing in a liquid phase. In either case, the person of skill in the art will be able to test using routine skill and knowledge whether any selected sequence derived from a PERV-B env gene is able to hybridise to the PERV-B env nucleic acid under conditions in which it is substantially unable to hybridise to PERV-A env nucleic acid, and vice versa.

One way to calculate T_m of a probe is by reference to the formula for calculating the T_m of probes to a homologous target sequence. This formula is $T_m(^{\circ}C) = 2(A+T) + 4(G+C) - 5$. This will provide the T_m under conditions of 3xSSC and 0.1% SDS (where SSC is 0.15M NaCl, 0.015M sodium citrate, pH 7). This formula is generally suitable for probes of up to 30 nucleotides in length. In the present invention, this formula may be used as an algorithm to calculate a nominal T_m of a probe for a specified sequence based upon the number of matches to its PERV target (e.g. PERV-B) sequence and PERV non-target sequence (e.g. PERV-A). For example, for the probe of SEQ ID NO:7 has a T_m of $((2 \times 11) + (4 \times 9) - 5) = 53^{\circ}C$. The sequence of SEQ ID NO:7 is derived from SEQ ID NO:3 and thus will have this T_m when used as a probe for this sequence, subject to the usual experimental error. However when SEQ ID NO:7 is used as a probe for the corresponding region of SEQ ID NO:1 (represented above as SEQ ID NO:9), the calculated T_m will be $((2 \times 9) + (4 \times 5) - 5) = 33^{\circ}C$, based on counting the

number of matches. (Since for the purposes of the present invention the above formula is used as an algorithm, the actual T_m of probes when hybridised to non-complementary targets which do not exactly match the probe sequence may or 5 may not correspond to the calculated value.)

Thus in a preferred aspect, a PERV-B specific probe will have a T_m (calculated as above) for SEQ ID NO:3 which is at least 5°C higher than for SEQ ID NO:1, and vice versa for a PERV-A specific probe. Preferably the difference is at least 8°C, 10 more preferably at least 10°C, at least 15°C or at least 20°C.

The above formula generally useful for probes up to 30 nucleotides in length, but since it is used simply as an algorithm in the present invention, it may be extended to longer probes, for example up to 40 or even up to 50 15 nucleotides in length.

Suitable conditions for a probe to hybridise to a PERV target sequence may also be measured experimentally. Suitable experimental conditions comprise hybridising a candidate probe to both SEQ ID NO:1 and SEQ ID NO:3 on a solid support under 20 low stringency hybridising conditions (e.g. 6xSSC at 55°C), washing at reduced SSC and/or higher temperature, for example at 0.2xSSC at 45°C, and increasing the hybridisation temperature incrementally to determine hybridisation conditions which allow the probe to hybridise to SEQ ID NO:1 25 but not SEQ ID NO:3, or vice versa, as the case may be.

Although the hybridisation conditions used to distinguish between the PERV-B and PERV-A env genes should also be sufficient to distinguish over other "background" sequences present in human or porcine cells (particularly human and 30 porcine genomic and mitochondrial sequences), it is also desirable that the probes do not, under such conditions, hybridise to such background sequences. This may also be determined by experiment, for example by blotting the probes

to a solid support which carries at separate loci SEQ ID NO:1, SEQ ID NO:3 (for example cloned in plasmids), human total DNA and porcine total DNA.

5 The size of the probe may be selected by those of skill in the art taking account of the particular purposes the probes are to be used. Probes may be for example from 10 to 1000 nucleotides (or base pairs), e.g. from 50 to 500, such as from 200 to 500 nucleotides or base pairs. This size range is particularly suitable for Southern blots. However for some 10 purposes, for example PCR, short oligonucleotide probes are preferred, generally in the size range of from 10 to 40 nucleotides in length, preferably 12 to 25 and more preferably from 18 to 24 such as 20, 21 or 22 nucleotides.

15 The probes may be labelled with a detectable label, including a radionuclide such as ^{32}P or ^{35}S which can be added to the probe using methods known per se in the art. The probe may alternatively carry a non-radioactive label such as biotin.

20 Generally, probes will be prepared by stepwise chemical synthesis, which is widely available commercially.

25 Recombinant production of probes is also possible. Probes may be DNA or RNA, and may contain or consist of synthetic or modified nucleotides. A number of different types of modification to oligonucleotides are known in the art. These include methylphosphonate and phosphorothionate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the probes and primers described herein may be modified by any method available in the art.

30 A preferred method of detection is by the polymerase chain reaction (PCR). This will involve PERV-B or PERV-A primer pairs, at least one of which is directed to PERV-B or PERV-A env gene sequences, the polarity of the probes being such that

the region between them is amplified when the PCR is performed. At least one of each pair of PERV-A and/or PERV-B primers will be specific for its target PERV sequence. The other member of each pair may be targeted to non-env sequence or env sequence common to PERV-A and PERV-B. Preferably both members of a primer pair are specific for their target PERV sequence. Desirably the probes will be selected to amplify a region of the PERV-A and PERV-B of a convenient size to detect, such as between about 50 and 500, preferably between 150 and 400 nucleotides.

Where pairs of PERV-A and PERV-B primers are used in conjunction with each other, it is preferred that the primer pairs are selected such that different size PERV-A and PERV-B products are produced. Preferably the difference in size is at least from 5 to 50 base pairs, such as from 10 to 25 base pairs, so that detection of the products by electrophoresis on agarose gels by ethidium bromide staining may be conveniently carried out.

The methods of the invention which allow the PERV-A and PERV-B subtypes to be distinguished are useful in following the transmission of these viruses from porcine cells to other cell types, particularly human cells. In addition, the probes may be used to clone and characterize the different endogenous proviruses of pigs. Specific proviruses can be characterised by both their sequences and the genomic flanking sequences, and thus a map of the chromosomal locations of the viruses may be determined. The ability to distinguish between PERV-A and PERV-B proviruses will facilitate studies of the porcine endogenous retroviruses which might pose a threat to humans in a transplant setting.

The PERV-A and PERV-B nucleic acid sequences of the invention are novel and thus in a further aspect of the invention there is provided an isolated nucleic acid consisting essentially of the PERV-A or PERV-B env gene coding sequence, or a fragment

thereof which is capable of hybridising to the PERV-B env gene under conditions in which said probe is substantially unable to hybridise to the PERV-A env gene, or vice versa. Vectors which comprise such sequences form a further aspect of the invention. The vector may be for replication of the sequence or for expression of the sequence in a suitable host cell. In such a case the vector will comprise a promoter operably linked to the env sequence, the promoter being compatible with the host cell which may be, for example, bacterial, e.g. *E.coli*, yeast, insect or mammalian, e.g. a CHO cell or a human cell line.

The env gene may be expressed in such a cell and recovered from the cell in substantially isolated form.

The differences in the PERV subtypes also allow the production of antibodies which can distinguish between the two subtypes. In a manner analogous to the production of probes, the sequence differences between the proteins of SEQ ID NO. 2 and SEQ ID NO. 4 can be examined, and suitable epitopes which reflect these differences determined using computer algorithms or by epitope scanning techniques. Monoclonal antibodies raised against these epitopes may be used to detect the presence of the PERV-A and/or PERV-B subtypes in a specific manner.

In a manner analogous to the nucleic acid probes, the antibodies are preferably directed to epitopes in the N-terminal region of the PERV-A and PERV-B env proteins, particularly epitopes encoded within the preferred regions identified above.

For the purposes of the present invention the term antibody describes an immunoglobulin whether natural or partly or wholly synthetically produced. The term also covers any polypeptide or protein having a binding domain which is, or is homologous to, an antibody binding domain. These can be

derived from natural sources, or they may be partly or wholly synthetically produced. Examples of antibodies are the immunoglobulin isotypes and their isotypic subclasses; fragments which comprise an antigen binding domain such as 5 Fab, scFv, Fv, dAb, Fd; and diabodies.

It is possible to take monoclonal and other antibodies and use techniques of recombinant DNA technology to produce other antibodies or chimeric molecules which retain the specificity of the original antibody. Such techniques may involve 10 introducing DNA encoding the immunoglobulin variable region, or the complementarity determining regions (CDRs), of an antibody to the constant regions, or constant regions plus framework regions, of a different immunoglobulin. See, for instance, EP-A-184187, GB 2188638A or EP-A-239400. A 15 hybridoma or other cell producing an antibody may be subject to genetic mutation or other changes, which may or may not alter the binding specificity of antibodies produced.

As antibodies can be modified in a number of ways, the term "antibody" should be construed as covering any specific 20 binding member or substance having a binding domain with the required specificity. Thus, this term covers antibody fragments, derivatives, functional equivalents and homologues of antibodies, including any polypeptide comprising an immunoglobulin binding domain, whether natural or wholly or 25 partially synthetic. Chimeric molecules comprising an immunoglobulin binding domain, or equivalent, fused to another polypeptide are therefore included. Cloning and expression of chimeric antibodies are described in EP-A-0120694 and EP-A-0125023.

30 It has been shown that fragments of a whole antibody can perform the function of binding antigens. Examples of binding fragments are (i) the Fab fragment consisting of VL, VH, CL and CH1 domains; (ii) the Fd fragment consisting of the VH and CH1 domains; (iii) the Fv fragment consisting of the VL and VH

domains of a single antibody; (iv) the dAb fragment (Ward, E.S. et al., *Nature* 341, 544-546 (1989)) which consists of a VH domain; (v) isolated CDR regions; (vi) F(ab')₂ fragments, a bivalent fragment comprising two linked Fab fragments (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by a peptide linker which allows the two domains to associate to form an antigen binding site (Bird et al, *Science*, 242, 423-426, 1988; Huston et al, *PNAS USA*, 85, 5879-5883, 1988); (viii) bispecific single chain Fv dimers (PCT/US92/09965) and (ix) "diabodies", multivalent or multispecific fragments constructed by gene fusion (WO94/13804; P. Holliger et al *Proc. Natl. Acad. Sci. USA* 90 6444-6448, 1993).

The reactivities of antibodies to an epitope in a sample may be determined by any appropriate means. Tagging with individual reporter molecules is one possibility. The reporter molecules may directly or indirectly generate detectable, and preferably measurable, signals. The linkage of reporter molecules may be directly or indirectly, covalently, eg via a peptide bond or non-covalently. Linkage via a peptide bond may be as a result of recombinant expression of a gene fusion encoding antibody and reporter molecule.

One favoured mode is by covalent linkage of each antibody with an individual fluorochrome, phosphor or laser dye with spectrally isolated absorption or emission characteristics. Suitable fluorochromes include fluorescein, rhodamine, phycoerythrin and Texas Red. Suitable chromogenic dyes include diaminobenzidine. Other reporters include macromolecular colloidal particles or particulate material such as latex beads that are coloured, magnetic or paramagnetic, and biologically or chemically active agents that can directly or indirectly cause detectable signals to be visually observed, electronically detected or otherwise recorded. These molecules may be enzymes which catalyse

reactions that develop or change colours or cause changes in electrical properties, for example. They may be molecularly excitable, such that electronic transitions between energy states result in characteristic spectral absorptions or 5 emissions. They may include chemical entities used in conjunction with biosensors. Biotin/avidin or biotin/streptavidin and alkaline phosphatase detection systems may be employed.

10 A radionuclide such as ^{125}I , ^{111}In or $^{99\text{m}}\text{Tc}$ may be attached to an antibody and these nuclides are useful in imaging target antigens in the body. Antibodies labelled with these labels may be used to examine xenotransplanted organs in a human recipient for the presence of PERVs as part of ongoing monitoring following transplantation.

15 Antibodies of the invention may be produced by conventional hybridoma technology, e.g by linking a peptide comprising a suitable epitope to a carrier protein, injecting the linked peptide into an animal such as a rat or rabbit, recovering the spleen and producing hybridoma cell lines which are screened 20 against the peptide for specific binding. Antibodies may also be prepared by screening against synthetic libraries such as phage display libraries. Antibodies may also be made against the entire env protein or substantial parts thereof, and then screened individually against PERV-A and PERV-B env protein 25 for specific binding to one or the other.

30 In one aspect of the invention a specific PERV-A antibody and a specific PERV-B antibody are used on parallel samples (or on the same sample where the two antibodies are labelled with different and distinguishable labels) to detect the presence of the two subtypes of retroviruses.

Antibodies specific for a PERV-B epitope will have at least a 100 fold higher affinity for that epitope than for the corresponding region (as indicated by alignments to the PERV-A

sequence such as that of Figure 1) of the PERV-A env protein., and vice versa. Desirably both types of specific antibodies will not cross react to other proteins normally present in human and porcine cells (i.e. have at least a 100 fold higher affinity to its target epitope than to such other proteins).

5 The probes, primers and antibodies of the invention may be used in all aspects of the development of porcine organ (e.g. kidney, liver, heart, pancreas, including tissues and cells therefrom, such as pancreatic islet cells) xenotrans-
10 plantation. Thus the probes, primers and antibodies may be used to monitor the inheritance of human tropic viruses, thus facilitating the breeding of pigs lacking these viruses, particularly the PERV-B subtype. The invention will also be useful in monitoring the expression of the viruses in pigs and
15 humans.

The following examples illustrate the invention.

Example 1: Cloning of PERV-A and PERV-B Env sequences.

20 cDNA clones were obtained using the 3' RACE technique (Frohman and Martin Technique 1:165-170, 1989). Total RNA from PK15, MPK and 293 cells was reverse transcribed to produce cDNA using an adapter primer dT-Ri-Ro.

25 A fraction of cDNA from PK15 and MPK cells was amplified by the polymerase chain reaction (PCR) using the primer PL146 (5'ATCCGTCGGCATGCATAATACGACTCAC, SEQ ID NO:11) in combination with PL135 (5'CGATTCACTGCTGCTACAAAC, SEQ ID NO:12) or PL137 (5'CCCTTATAACCTCTTGAGCG, SEQ ID NO:13). Products of approximately 6.5 kb were digested with *Xba*I and *Sph*I and cloned into *Sal*I//*Sph*I digested pGem3Zf(+). Positive clones were identified and sequenced.

30 A portion of cDNA from 293 cells was amplified by PCR using primer PL137 in combination with primer Ro. Products of

approximately 6.5 kb were isolated and digested with *Pst*I and ligated with the pGem3Zf(+) plasmid digested with *Pst*I and *Sma*I. After transformation into *E.coli*, positive clones were identified and sequenced.

5 Further clones were generated and sequenced from MPK and PK15 cDNA by amplification with primer PL147 (5'GTAATGCATGCTTCTATGGTGCCAGTCG, SEQ ID NO:14) in combination with either PL135, PL137 or PL148 (5'CTCTACGCATGCGTGGTGTACGACTGTG, SEQ ID NO:15) and digestion of products with *Xho*I/*Sph*I or *Sph*I and cloning into appropriately digested pGEM3Zf(+) .

10

Further clones were generated and sequenced from 293 cDNA by PCR amplification with primer PL147 in combination with either PL135, PL137 or PL149 (5'GTAATCGGGTCAGACAATGG, SEQ ID NO:16) and digestion of products with *Eco*RI/*Pst*I, *Pst*I, or *Bam*HI/*Eco*RI and cloning into appropriately digested pGem3Zf(+) .

15 Oligos dT-Ri-Ro and Ro come from Frohman and Martin (Technique 1:165-170, 1989), PL146 is a modified version of Ro containing an additional *Sph*I site, PL135 and PL137 were designed from the published PERV pol sequence (Tristan et al J.Virol 70:8241-8246, 1996 Genbank ID X99933), PL147 and PL148 are PERV LTR primers derived from the sequences of our initial 293 clones.

20 25 Analysis of the clones identified two distinct subtypes, which we have termed PERV-A and PERV-B. An alignment of the two subtype envelope gene sequences is shown in Figure 1.

Example 2: Frequency of full length PERV-A and PERV-B env gene isolation.

30 The frequency of the subtypes in pig and human cells was analysed and the results are as follows:

1. From pig PK-15 cells

29/32 PERV-A 3/32 PERV-B

2. From human 293 cells infected with PK15 virus

0/18 PERV-A 18/18 PERV-B

5

Example 3: Preparation of specific probes

1. PCR

Differences between the PERV-A and PERV-B subgroups allow the design of specific primers

PL170 TGGAAAGATTGGCAACAGCG (SEQ ID NO:5)

10 PL171 AGTGATGTTAGGCTCAGTGG (SEQ ID NO:6)

PL172 TTCTCCTTGTCAATTCCGG (SEQ ID NO:7)

PL173 TACTTTATCGGGTCCCACTG (SEQ ID NO:8)

PL170+PL171 are predicted to give a 361 base pair band with PERV-A;

15 PL172+PL173 are predicted to give a 264 base pair band with PERV-B. PCR studies with cloned plasmid DNA confirmed these prediction and showed no cross-amplification between the two primer pairs. Sequencing the respective RT-PCR products from RNA containing both viral RNAs shows amplification only of the sequences predicted from each primer pair.

2. Southern blot probes.

The amplification products of PL170+PL171 (361 bp, PERV-A probe) and PL172+PL173 (264 bp, PERV-B probe) show no cross hybridisation on plasmid blots. Both have been used on genomic southern blots.

Example 4: Host range studies

The host range specified by the cloned PERV env genes were examined using a Moloney murine leukemia virus (Mo-MLV) based vector to deliver the β -galactosidase (lacZ) indicator gene to different cell types (Tailor et al J.Virol. 67:6737-6741,

1993). The TELCeB6 cell line (Cosset et al J.Virol. 69: 7430-7436, 1995) is derived from TE671 cells by stable transfection with CeB to supply the Mo-MLV gag-pol genes and carrying a modified lacZ gene (Ferry et al PNAS 88: 8377-8381, 1991) in proviral context introduced by infection using an amphotropic viral vector. The PERV env genes were introduced by transfection of TELCeB6 cells with expression constructs derived from pFBMOSALF (Cosset et al J.Virol. 69: 6314-6322, 1995) in which the PERV sequences, on XbaI-ClaI fragments, 5 replace the corresponding Mo-MLV envelope sequence. Virus produced by transiently and stably transfected TELCeB6 cells were assayed for transfer of LacZ on 293, TE671 (human) and 10 PK-15, PAE, ST-IOWA (pig) cells. Transfer of retroviral particles comprising the PERV-B envelope to human cells was 15 demonstrated.

The infectious titre (LacZ positives/ml supernatant) was as follows:

	Pig (ST-IOWA)	Mink (Mu-1-lv)	Human (293)	Human (TE671)
Virus				
PERV-A	2000	1000	300	2000
PERV-B	800	4000	800	700

SEQUENCE LISTING

SEQ ID NO. 1: PERV-A.seq

TCGAGTGGGT GAGGCAGCGA GCGTGGAAAGC AGCTCCGGGA GGCCTACTCA
 GGAGGAGACT TGCAAGTTCC ACATCGCTTC CAAGTTGGAG ATTCAAGTCTA 100
 TGTAGACGC CACCGTGCAG GAAACCTCGA GACTCGGTGG AAGGGACCTT
 ATCTCGTACT TTTGACCACA CCAACGGCTG TGAAAGTCGA AGGAATCCCC 200
 ACCTGGATCC ATGCATCCCA CGTTAAGCCG GCGCCACCTC CCGATTGGGG
 GTGGAAAGCC GAAAAGACTG AAAATCCCCCT TAAGCTTCGC CTCCATCGCG 300
 TGGTTCCCTTA CTCTGTCAAT AACTCCTCAA GTTAATGGTA AACGCCTTGT
 GGACAGCCCCG AACTCCCCATA AACCCCTTATC TCTCACCTGG TTACTTACTG 400
 ACTCCGGTAC AGGTATTAAT ATTAACAGCA CTCAAGGGGA GGCTCCCTTG
 GGGACCTGGT GGCTGAATT ATATGTCTGC CTTCGATCAG TAATCCCTGG 500
 TCTCAATGAC CAGGCCACAC CCCCCGATGT ACTCCGTGCT TACGGGTTTT
 ACGTTTGCCCC AGGACCCCCA AATAATGAAG AATATTGTGG AAATCCTCAG 600
 GATTTCCTTT GCAAGCAATG GAGCTGCATA ACTTCTAATG ATGGGAATTG
 GAAATGGCCA GTCTCTCAGC AAGACAGAGT AAGTTACTCT TTTGTTAACCA 700
 ATCCTACCAAG TTATAATCAA TTTAATTATG GCCATGGGAG ATGGAAAGAT
 TGGCAACAGC GGGTACAAAA AGATGTACGA AATAAGCAAA TAAGCTGTCA 800
 TTCGTTAGAC CTAGATTACT TAAAAATAAG TTTCACTGAA AAAGGAAAAC
 AAGAAAATAT TCAAAAGTGG GTAAATGGTA TATCTTGGGG AATAGTGTAC 900
 TATGGAGGCT CTGGGAGAAA GAAAGGATCT GTTCTGACTA TTCCGCCTCAG
 AATAGAAAAT CAGATGGAAC CTCCGGTTGC TATAGGACCA AATAAGGGTT 1000
 TGGCCGAACA AGGACCTCCA ATCCAAGAAC AGAGGCCATC TCCTAACCCCC
 TCTGATTACA ATACAACCTC TGGATCAGTC CCCACTGAGC CTAACATCAC 1100
 TATTAAAACA GGGGCGAAAC TTTTTAGCCT CATCCAGGGA GCTTTCAAG
 CTCTTAACCTC CACGACTCCA GAGGCTACCT CTTCTTGTG GCTTTGCTTA 1200
 GCTTCGGGCC CACCTTACTA TGAGGGAATG GCTAGAGGAG GGAAATTCAA
 TGTGACAAAG GAACATAGAG ACCAATGTAC ATGGGGATCC CAAAATAAGC 1300
 TTACCCCTTAC TGAGGTTTCT GGAAAAGGCA CCTGCATAGG GATGGTTCCC
 CCATCCCACC AACACCTTTG TAACCACACT GAAGCCTTAA ATCGAACCTC 1400
 TGAGAGTCAA TATCTGGTAC CTGGTTATGA CAGGTGGTGG GCATGTAATA
 CTGGATTAAC CCCTTGTGTT TCCACCTTGG TTTTCAACCA AACTAAAGAC 1500
 TTTTGCCTTA TGGTCCAAAT TGTCCCCCGG GTGTACTACT ATCCCGAAAA
 AGCAGTCCTT GATGAATATG ACTATAGATA TAATCGGCCA AAAAGAGAGC 1600
 CCATATCCCT GACACTAGCT GTAATGCTCG GATTGGGAGT GGCTGCAGGC
 GTGGGAACAG GAACGGCTGC CCTAATCACA GGACCGCAAC AGCTGGAGAA 1700
 AGGACTTAGT AACCTACATC GAATTGTAAC GGAAGAGATCTC CAAGCCCTAG

AAAAATCTGT CAGTAACCTG GAGGAATCCC TAACCTCCTT ATCTGAAGTG 1800
 GTTCTACAGA ACAGAAGGGG GTTAGATCTG TTATTTCTAA AAGAAGGAGG
 GTTATGTGTA GCCTTAAAAG AGGAATGCTG CTTCTATGTA GATCACTCAG 1900
 GAGCCATCAG AGACTCCATG AGCAAGCTTA GAGAAAGGTT AGAGAGGCCT
 CGAAGGGAAA GAGAGGCTGA CCAGGGGTGG TTTGAAGGAT GGTCAACAG 2000
 GTCTCCTTGG ATGACCACCC TGCTTCTGC TCTGACGGGG CCCCTAGTAG
 TCCTGCTCCT GTTACTTACA GTTGGGCCTT GCTTAATTAA TAGGTTGTT 2100
 GCCTTTGTTA GAGAACGAGT GAGTGCAGTC CAGATCATGG TACTTAGGCA
 ACAGTACCAA GGCCTTCTGA GCCAAGGAGA AACTGACCTC TAGCCTTCCC 2200
 AGTTCTAAGA TTAGAACTAT TAACAAGACA AGAAGTGGGG AATGAAAGGA
 TGAAAATGCA ACCTAACCC CCCAGAACCC AGGAAGTTAA TAAAAAGCTC 2300
 TAAATGCCCC CGAATTCCAG ACCCTGCTGG CTGCCAGTAA ATAGGTAGAA
 GGTACACATT CCTATTGTT CAGGGCCTGC TATCCTGGCC TAAGTAAGAT 2400
 AACAGGAAAT GAGTTGACTA ATCGCTTATC TGGATTCTGT AAAACCGACT
 GGCACCATAG AA

2462

SEQ ID NO. 2: Translation of PERV-A env (1 letter code)

MHPTLSRRHLPPIRGK PKRLKIPLSFASIAWF LTLSITPQVNGKRLVD 48
 SPNSHKPLSLTWLLTD SGTGININSTQGEAPL GTWWPELYVCLRSVIP 96
 GLNDQATPPDVLRAYG FYVCPGPPNNEEYCGN PQDFFCKQWSCITSND 144
 GNWKWPVSQQDRVSYS FVNNPTSYNQFNYGHG RWKDWQQRVQKDVRNK 192
 QISCHSLLDYLIKSF TEKGKQENIQKWVNGI SWGIVYYGGSGRKKGS 240
 VLTIRLRIETQMEPPV AIGPNKGLAEQGPPIQ EQRPSPNPSDYNTTSG 288
 SVPTEPNITIKTGAKL FSLIQGAFQALNSTTP EATSSCWLCASGPPY 336
 YEGMARGGKFNVTKEH RDQCTWGSQNKLTLTE VSGKGTICIGMVPSSHQ 384
 HLCNHTEAFNRTSESQ YLVPGYDRWWACNTGL TPCVSTL VFNQTKDFC 432
 VMVQIVPRVYYPEKA VLDEYDYRYNRPKREP ISLTLAVMLGLGVAAG 480
 VGTGTAALITGPQQLE KGLSNLHRIVTEDLQA LEKSVSNLEESLTSLS 528
 EVVLQNRRGLLLFLK EGGLCVALKEECCFYV DHSGAIRDSMSKLRER 576
 LERRRREREADQGWFE GWFNRSPWMTTLSAL TGPLVVVLLLLTVGPC 624
 LINRFVAFVREVRSAV QIMVLRQQYQGLLSQG ETDL* 660

SEQ ID NO. 3: PERV-B.seq

GCATGCCTGC AGCAGTTGGT CAGAACATCC CCTTATCATG TTCTGAGGCT
 ACCAGGAGTG GCTGACTCGG TGGTCAAACA TTGTGTGCCG TGCCAGCTGG 100

TTAATGCTAA TCCTTCCAGA ATACCTCCAG GAAAGAGACT AAGGGGAAGC
 CACCCAGGGC CTCACTGGGA AGTGGACTTC ACTGAGGTAA AGCCGGCTAA 200
 ATACGGAAAC AAATATCTAT TGTTTTGT AGACACCTTT TCAGGATGGG
 TAGAGGCTTA TCCTACTAAG AAAGAGACTT CAACCGTGGT GGCTAAAAAA 300
 ATACTGGAGG AAATTTTCC GAGATTGGA ATACCTAAGG TAATCGGGTC
 AGACAATGGT CCAGCTTTG TTGCCAGGT AAGTCAGGGA CTGGCCAAGA 400
 TATTGGGGAT TGATTGGAAA CTGCATTGTG CATAACAGACC CCAAAGCTCA
 GGACAGGTAG AGAGGATGAA TAGAACCATT AAAGAGACCC TTACCAAATT 500
 GACCACAGAG ACTGGCATTAA ATGATTGGAT AGCTCTCCTG CCCTTTGTGC
 TTTTAGGGT TAGGAACACC CCTGGACAGT TTGGGCTGAC CCCCTATGAA 600
 TTGCTCTACG GGGGACCCCC CCCGTTGGTA GAAATTGCTT CTGTACATAG
 TGCTGATGTG CTGCTTTCCC AGCCTCTGTT CTCTAGGCTC AAGGCGCTCG 700
 AGTGGGTGAG GCAACGAGCG TGGAAAGCAGC TCCGGGAGGC CTACTCAGGA
 GAAGGAGACT TGCAAGTTCC ACATCGCTTC CAAGTGGGAG ATTCAAGTCTA 800
 TGTTAGACGC CACCGTGCAG GAAACCTCGA GACTCGGTGG AAGGGCCCTT
 ATCTCGTACT TTTGACCACA CCAACGGCTG TGAAAGTCGA AGGAATCTCC 900
 ACCTGGATCC ATGCATCCCA CGTTAAGCTG GCGCCACCTC CCGACTCGGG
 GTGGAGAGCC GAAAAGACTG AGAATCCCC TAAGCTTCGC CTCCATCGCC 1000
 TGGTTCTTA CTCTAACAAAT AACTCCCCAG GCCAGTAGTA AACGCCTTAT
 AGACAGCTCG AACCCCCATA GACCTTATC CCTTACCTGG CTGATTATTG 1100
 ACCCTGATAC GGGTGTCACT GTAAATAGCA CTCGAGGTGT TGCTCCTAGA
 GGCACCTGGT GGCCTGAAC GCATTTCTGC CTCCGATTGA TTAACCCCCGC 1200
 TGTTAAAAGC ACACCTCCCA ACCTAGTCCG TAGTTATGGG TTCTATTGCT
 GCCCAGGCAC AGAGAAAAGAG AAATACTGTG GGGGTTCTGG GGAATCCTTC 1300
 TGTAGGAGAT GGAGCTGCGT CACCTCCAAC GATGGAGACT GGAAATGGCC
 GATCTCTCTC CAGGACCGGG TAAAATTCTC CTTTGTCAAT TCCGGCCCGG 1400
 GCAAGTACAA AGTGATGAAA CTATATAAAG ATAAGAGCTG CTCCCCATCA
 GACTTAGATT ATCTAAAGAT AAGTTCACT GAAAAAGGAA AACAGGAAAA 1500
 TATTCAAAAG TGGATAAAATG GTATGAGCTG GGGAAATAGTT TTTTATAAAT
 ATGGCGGGGG AGCAGGGTCC ACTTTAACCA TTGCGCTTAG GATAGAGACG 1600
 GGGACAGAAC CCCCTGTGGC AGTGGGACCC GATAAAAGTAC TGGCTGAACA
 GGGGCCCCCG GCCCTGGAGC CACCGCATAA CTTGCCGGTG CCCCATTAA 1700
 CCTCGCTGCG GCCTGACATA ACACAGCCGC CTAGCAACGG TACCACTGGA
 TTGATTCTTA CCAACACGCC TAGAAACTCC CCAGGTGTTG CTGTTAAGAC 1800
 AGGACAGAGA CTCTTCAGTC TCATCCAGGG AGCTTTCCAA GCCATCAACT
 CCACCGACCC TGATGCCACT TCTTCTTGTT GGCTTTGTCT ATCCTCAGGG 1900
 CCTCCTTATT ATGAGGGGAT GGCTAAAGAA GGAAAATTCA ATGTGACCAA

AGAGCATAGA AATCAATGTA CATGGGGTC CCGAAATAAG CTTACCCCTCA 2000
 CTGAAGTTTC CGGGAAAGGGG ACATGCATAG GAAAAGCTCC CCCATCCCAC
 CAACACCTT GCTATAGTAC TGTGGTTAT GAGCAGGCCT CAGAAAATCA 2100
 GTATTTAGTA CCTGGTTATA ACAGGGTGGT GGCATGCAAT ACTGGGTTAA
 CCCCTGTGT TTCCACCTCA GTCTCAACC AATCCAAAGA TTTCTGTGTC 2200
 ATGGTCCAAA TCGTCCCCCG AGTGTACTAC CATCCTGAGG AAGTGGTCCT
 TGATGAATAT GACTATCGGT ATAACCGACC AAAAAGAGAA CCCGTATCCC 2300
 TTACCCCTAGC TGTAATGCTC GGATTAGGGA CGGCCGTGG CGTAGGAACA
 GGGACAGCTG CCCTGATCAC AGGACCACAG CAGCTAGAGA AAGGACTTGG 2400
 TGAGCTACAT CGGGCCATGA CAGAAGATCT CCGAGCCTTA GAGGAGTCTG
 TTAGCAACCT AGAAGAGTCC CTGACTTCTT TGTCTGAAGT GGTTCTACAG 2500
 AACCGGAGGG GATTAGATCT GCTGTTCTA AGAGAAGGTG GGTTATGTGC
 AGCCTTAAAAA GAAGAATGTT GCTTCTATGT AGATCACTCA GGAGCCATCA 2600
 GAGACTCCAT GAGCAAGCTT AGAGAAAGGT TAGAGAGGCG TCGAAGGGAA
 AGAGAGGCTG ACCAGGGGTG GTTGAAGGA TGGTTCAACA GGTCTCCTTG 2700
 GATGACCACC CTGCTTCTG CTCTGACGGG ACCCCTAGTA GTCCTGCTCC
 TGTTACTTAC AGTTGGGCCT TGCTTAATTA ATAGGTTTGT TGCCTTTGTT 2800
 AGAGAACGAG TGAGTGCAGT CCAGATCATG GTACTTAGGC AACAGTACCA
 AGGCCTCTG AGCCAAGGAG AAAC TGACCT CTAGCCTTCC CAGTTCTAAG 2900
 ATTAGAACTA TTAACAAGAC AAGAAGTGGG GAATGAAAGG ATGAAAATGC
 AACCTAACCC TCCCAGAACCC CAGGAAGTTA ATAAAAAGCT CTAAATGCC 3000
 CCGAATTCCA GACCCTGCTG GCTGCCAGTA AATAGGTAGA AGGTCACACT
 TCCTATTGTT CCAGGGCCTG CTATCCTGGC CTAAGTAAGA TAACAGGAAA 3100
 TGAGTTGACT AATCGCTTAT CTGGATTCTG TAAAACCGAC TGGCACCATA
 GAAGAATTGA TTACACATTG ACAGCCCTAG TGACCTATCT CAACTGCAAT 3200
 CTGTCACTCT GCCCAGGAGC CCACGCAGAT GCGGACCTCC GGAGCTATT
 TAAAATGATT GGTCCACCGGA GCGCGGGCTC TCGATATTTT AAAATGATTG 3300
 GTCCACGGAG CGCGGGCTCT TCGATATTTT AAAATGATTG GTTGTGACCG
 CACAGGCTTT GTTGTGAACC CCATAAAAGC TGTCCCGATT CCGCACTCGG 3400
 GGCCGCAGTC CTCTACCCCT GCGTGGTGTGTA CGACTGTGGG CCCCAGCGCG
 CTTGGAATAA AAATCCTCTT GCTGTTGCA TC

3482

SEQ ID NO. 4: Translation of PERV-B env (1 letter code)
 MHPTLSWRHLPTRGGE PKRLRIPLSFASIAWF LTLTITPQASSKRLID 48
 SSNPHRPLSLTWLIID PDTGVTVNSTRGVAPR GTWWPELHFCLRLINP 96
 AVKSTPPNLVRSYGFY CCPGTEKEKYCGGSGE SFCRRWSCVTSNDGDW 144
 KWPISLQDRVKFVNSP VNSP SGPGKYKVMKLYKD KS P S D L D Y L K I S F T E K 192

GKQENIQKWINGMWSW IIVFYKYGGGAGSTLTI RLRIETGTEPPVAVGP 240
 DKVLAEQGPPALEPPH NLPVPQLTSLRPDITQ PPSNGTGLIPTNTPR 288
 NSPGPVVKTGQRLFSL IQGAFQAINSTDPDAT SSCWLCLSSGPPYYEG 336
 MAKEGKFNVTKEHRNQ CTWGSRNKLTLEEVSG KGTCIGKAPPQHQHLC 384
 YSTVVYEQASENQYLV PGYNRWWACNTGLTPC VSTSVFNQSKDFCVMV 432
 QIVPRVYYHPEEVVLD EYDYRYNRPKREPVS LTLAVMLGLGTAVGVGT 480
 GTAALITGPQQLEKGL GELHAAMTEDLRALEE SVSNLEESLTSLSSEVV 528
 LQNRRGLDLLFLREGG LCAALKEECCFYVDHS GAIIRDMSKLRERLER 576
 RRREREADQGWFEGLWF NRSPWMTTLLSALTGP LVVLLLLLTVGPCLIN 624
 RFVAFVRERVSAVQIM VLRQQYQGLLSQGETD L* 657

SEQ ID NO:5

TGGAAAGATTGGCAACAGCG (SEQ ID NO:5)

SEQ ID NO:6

AGTGATGTTAGGCTCAGTGG (SEQ ID NO:6)

SEQ ID NO:7

TTCTCCTTGTCAA--TTCCGG 3' (SEQ ID NO:7)

SEQ ID NO:8

TACTTTATCGGGTCCCACTG 3' (SEQ ID NO:8)

SEQ ID NO:9

TACTCTTTGTTAACAAATCCTA 3' (SEQ ID NO:9)

SEQ ID NO:10

TATTCTGAGGCGCGAATAGT 3' (SEQ ID NO:10)

SEQ ID NO:11

ATCCGTCGGCATGCATAATACGACTCAC (SEQ ID NO:11)

SEQ ID NO:12

CGATTCACTGCTGCTACAAC (SEQ ID NO:12)

SEQ ID NO:13

25

CCCTTATAACCTCTTGAGCG (SEQ ID NO:13)

SEQ ID NO:14

GTAATGCATGCTTCTATGGTGCCAGTCG (SEQ ID NO:14)

SEQ ID NO:15

CTCTACGCATGCGTGGTGTACGACTGTG (SEQ ID NO:15)

SEQ ID NO:16

GTAATCGGGTCAGACAATGG (SEQ ID NO:16)

CLAIMS

1. An isolated nucleic acid probe, said probe being capable of hybridising to the PERV-B env gene under conditions in which said probe is substantially unable to hybridise to the PERV-A env gene.
2. An isolated nucleic acid probe according to claim 1 which is capable of hybridising to SEQ ID NO:3 or the complement thereof under conditions in which it is not capable of hybridising to SEQ ID NO:1 or the complement thereof.
3. An isolated nucleic acid probe according to claim 1 or 2 which is derived from the region of PERV-B derived from nucleotides 1000 to 2500 of the SEQ ID NO. 3 isolate.
4. An isolated nucleic acid probe, said probe being capable of hybridising to the PERV-A env gene under conditions in which said probe is substantially unable to hybridise to the PERV-B env gene.
5. An isolated nucleic acid probe according to claim 4 which is capable of hybridising to SEQ ID NO:1 or the complement thereof under conditions in which it is not capable of hybridising to SEQ ID NO:3 or the complement thereof.
6. An isolated nucleic acid according to claim 4 or 5 which is derived from the region of PERV-A derived from nucleotides 300 to 1809 of the SEQ ID NO:1 isolate.
7. An isolated nucleic acid probe according to any one of the preceding claims which is from 10 to 40 nucleotides in length.
8. A pair of primers suitable for conducting a polymerase chain reaction, at least one of said primers being a nucleic acid as defined in any one of claims 1 to 3.

9. A pair of primers suitable for conducting a polymerase chain reaction, at least one of said primers being a nucleic acid as defined in any one of claims 4 to 6.

10. A method of determining the subtype of a porcine endogenous retrovirus in a sample which contains or is suspected to contain one or both of the PERV-A and PERV-B subtypes, said method comprising probing said tissue with a nucleic acid probe as defined in any one of claims 1 to 7, or by conducting a polymerase chain reaction with a pair of primers as defined in claim 8 or 9, and determining whether or not said probe or pair of primers detects either of said subtypes.

11. A method according to claim 10 wherein retroviral material from said cells is amplified prior to probing or conducting said PCR.

12. A method according to claim 10 wherein the sample is cloned nucleic acid obtained from pig or human cells.

13. A method according to claim 10 or 11 wherein the sample comprises tissue which is primary porcine tissue.

14. A method according to claim 10 or 11 wherein the sample of is a human cell line which has been cultivated in the presence of a porcine cell line.

15. An antibody capable of binding to an epitope on the PERV-B env protein under conditions where said antibody is substantially unable to bind to the PERV-A env protein.

16. An antibody capable of binding to an epitope on the PERV-A env protein under conditions where said antibody is substantially unable to bind to the PERV-B env protein.

17. A method of detecting the presence of a pig endogenous

retrovirus in porcine or human tissue or cell lines which comprises bringing a sample of said tissue or cell line into contact with an antibody according to claim 15 or 16 and detecting whether or not said antibody binds to a retrovirus in the sample.

18. Use of a probe according to any one of claims 1 to 7 in a method of determining the subtype of a porcine endogenous retrovirus.

PERV-A	10	20	30	40	50	60
	TCGAGTGGGTGAGGCAGCGAGCGTGGAAAGCAGCTCCGGAGGCCTACTCAGGAGGAGCT					
PERV-B	700	720	740		760	AGA
	A.....	
PERV-A	70	80	90	100	110	120
	TGCAAGTCCACATCGCTTCCAAGTTGGAGATTCACTATGTTAGACGCCACCGTGCAG					
PERV-B	780		800		820	
	G.....	
PERV-A	130	140	150	160	170	180
	GAAACCTCGAGACTCGGTGGAAAGGGACCTTATCTCGTACTTTGACCACACCAACGGCTG					
PERV-B	840		860		880	
	C.....	
PERV-A	190	200	210	220	230	240
	TGAAAGTCGAAGGAATCCCCACCTGGATCCATGCATCCCACGTTAACGCCGGCGCCACCTC					
PERV-B	900		920		940	
	T.....	T.....	
PERV-A	250	260	270	280	290	300
	CCGATTGGGTGGAAAGCCAAAAGACTGAAAATCCCTTAAGCTTCGCCTCCATCGCG					
PERV-B	960		980		1000	
C.....	G.....G.....C	
PERV-A	310	320	330	340	350	360
	TGGTTCTTACTCTGTCAATAACTCCTCAAGTTAACGCTTGTGGACAGCCCG					
PERV-B	1020		1040		1060	
AA.....C..G..CC..G..A.....A..A.....T..		
PERV-A	370	380	390	400	410	420
	AACTCCCATAAACCTTATCTCTCACCTGGTTACTTACTGACTCCGGTACAGGTATTAAT					
PERV-B	1080		1100		1120	
C.....	G....T....C..T....C..GA....T....C..T..A....G...G..C..C.				

Fig. 1a

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PERV-A	430	440	450	460	470	480
	ATTAACAGCACTCAAGGGAGGCTCCCTGGGACCTGGTGGCCTGAATTATATGCTGC					
PERV-B	1140			1160	1180	
	G.A..T.....G...T.TT.....TAGA..C.....C.GC..T.....					
PERV-A	490	500	510	520	530	540
	CTTCGATCAGTAATCCCTGGTCTCAATGACCAGGCCACACCCCCGATGTACTCCGTGCT					
PERV-B	1200			1220		
	..C....TGA.T.A...C.C.G.T.-----.T...A.CC..G....AG.					
PERV-A	550	560	570	580	590	600
	TACGGGTTTACGTTGCCAGGACCCCCAAATAATGAAGAATTGTGAAATCCTCAG					
PERV-B	1240	1260	1280			
	..T.....C..TTGC.....--.A..G.G..A..GA....C.....GGG.T..GG.					
PERV-A	610	620	630	640	650	660
	GATTCTTTGCAAGCAATGGAGCTGCATAACTCTAATGATGGAAATTGAAATGGCA					
PERV-B	1300	1320	1340			
	..A.C...C..T.G.AG.....G.C..C..C....AG.C.....G					
PERV-A	670	680	690	700	710	720
	GTCTCTCAGCAAGACAGAGTAAGTTACTCTTTGTTAACATCCTACCAAGTTATAATCAA					
PERV-B	1360	1380	1400			
	A.....TC..G...C.G....AA.T...C....C...-T...GG..C.GGCA.G....					
PERV-A	730	740	750	760	770	780
	TTTAATTATGCCATGGAGATGGAAAGATTGGCAACAGCGGGTACAAAAGATGTACGA					
PERV-B	1420	1440	1460			
	AG.G..G.-AA.T..TAA....-A.G..C.GCT.CC..T.-A.ACTT.G.TT..C..-A.					
PERV-A	790	800	810	820	830	840
	AATAAGCAAATAAGCTGTCATTCGTTAGACCTAGATTACTAAAAATAAGTTCACTGAA					
PERV-B	1480	1500	1520			
	G.....-TT.C....AA.AAG.AA.ACAGG.A.A..T.C.....A.GGT.-...C					

Fig. 1b

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PERV-A	850	860	870	880	890	900
	AAAGGAAAACAAGAAAATATTCAAAAGTGGTAAATGGTATATCTTGGGAATAGTGTAC					
			A			
PERV-B	1540	1560			1580	C
	TGG....T.GTTTTT...A.ATGGC.G...AGC.G...CC.CT..AACC.T.C.CT..G					
PERV-A	910	920	930	940	950	960
	TATGGAGGCTCTGGGAGAAAGAAAGGATCTGTTCTGACTATTGCCCTCAGAATAGAAACT					
PERV-B	1600		1620		1640	
	G..A...A.---...C...-...CCCC...GGCAGTGGGA.C.GAT.A.G..CTGG..					
PERV-A	970	980	990	1000	1010	1020
	CAGATGGAACCTCCGGTTGCTATAGGACCAAATAAGGGTTGGCGAACAGGACCTCCA					
PERV-B	1660		C	CTT		
	G.ACA..GG..C....-CC..GG..C...GC....CCGG..C..C..TT.--...G					
PERV-A	1030	1040	1050	1060	1070	1080
	ATCCAAGAACAGAGGCCATCTCCTAACCCCTCTGATTACAATACAACCTCTGGATCAGTC					
PERV-B	1720		1740			
	C.G.--.GC.T.----.AA.AC.G..G.----.G...CGGT...A.....TGA.T					
PERV-A	1090	1100	1110	1120	1130	1140
	CCCACTGAGCCTAACATCACTATTAAAACAGGGCGAAACTTTTAGCCTCATCCAGGGA					
PERV-B	1760		CAC AGA TCCCCAGGT			
	..T..CA.....G.TC..G....G....ACA..G...C..C..T.....					
PERV-A	1150	1160	1170	1180	1190	1200
	GCTTTCAAGCTTTAACCTCACGACTCCAGAGGCTACCTCTTGGCTTGCTTA					
PERV-B	1840		C			
C.....CA.C.....-T..T..C..T.....TC..					
PERV-A	1210	1220	1230	1240	1250	1260
	GCTTCGGGCCACCTTACTATGAGGAAATGGCTAGAGGAGGGAAATTCAATGTGACAAAG					
PERV-B	1900		1920		1940	
	T.C..A..G..T.....T.....G.....A..A..A.....C..A					

Fig. 1c

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PERV-A	1270	1280	1290	1300	1310	1320
	GAACATAGAGACCAATGTACATGGGATCCAAAATAAGCTTACCCCTTACTGAGGTTCT					
PERV-B	1960		1980		2000	
	..G.....A.T.....G....G.....C....A.....C					
PERV-A	1330	1340	1350	1360	1370	1380
	GGAAAAGGCACCTGCATAGGGATGGTCCCCATCCCACCAACACCTTTGTAACCACACT					
PERV-B	2020		2040		2060	
	..G..G..A.....A.AA.C.....CT.TAGT...					
PERV-A	1390	1400	1410	1420	1430	1440
	GAAGCCTTAATCGAACCTCTGAGAGTCATATCTGGTACCTGGTTATGACAGGTGGTGG					
PERV-B	2080		2100		2120	
	.TG.TT.A.G.G.AGG....A..A.A..G...T.A.....A.....					
PERV-A	1450	1460	1470	1480	1490	1500
	GCATGTAATACTGGATTAACCCCTTGTGTTCCACCTGGTTTCAACCAAACCTAAAGAC					
PERV-B	2140		2160		2180	
C.....G.....C.....CA..C.....T.C.....T					
PERV-A	1510	1520	1530	1540	1550	1560
	TTTGCGTTATGGTCCAAATTGTCCCCGGGTGTACTACTATCCGAAAAAGCAGTCCTT					
PERV-B	2200		2220		2240	
	..C..T..C.....C.....A.....C.....T..GG...TG.....					
PERV-A	1570	1580	1590	1600	1610	1620
	GATGAATATGACTATAGATATAATCGGCCAAAAGAGAGCCCATATCCCTGACACTAGCT					
PERV-B	2260		2280		2300	
C.G.....C..A.....A...G.....T..C.....					
PERV-A	1630	1640	1650	1660	1670	1680
	GTAATGCTCGGATTGGGAGTGGCTGCAGGCGTGGAACAGGAACGGCTGCCCTAATCACA					
PERV-B	2320		2340		2360	
A..GAC...C.TT....A.....G..A.....G.....					
PERV-A	1690	1700	1710	1720	1730	1740
	GGACCGAACAGCTGGAGAAAGGACTTAGAACCTACATCGAATTGTAACCGAAGATCTC					
PERV-B	2380		2400		2420	
A..G.....A.....G..G.G.....GCGGCCA.G..A.....					

Fig. 1d

SUBSTITUTE SHEET (rule 26)

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PERV-A	1750	1760	1770	1780	1790	1800
	CAAGCCCTAGAAAAATCTGTCAGTAACCTGGAGGAATCCCTAACCTCCTATCTGAAGTG					
PERV-B	2440	2460			2480	
	.G.....T....GG.G.....T..C.....A..A..G.....G..T..T..G.....					
PERV-A	1810	1820	1830	1840	1850	1860
	GTTCTACAGAACAGAACAGGGTTAGATCTGTTATTCTAAAAGAAGGAGGGTTATGTGTA					
PERV-B	2500	2520			2540	
C.G.....A.....C.G.....G.....T.....C.					
PERV-A	1870	1880	1890	1900	1910	1920
	GCCTTAAAAGAGGAATGCTGCTCTATGTAGATCACTCAGGAGCCATCAGAGACTCCATG					
PERV-B	2560	2580			2600	
A.....T.....					
PERV-A	1930	1940	1950	1960	1970	1980
	AGCAAGCTTAGAGAAAGGTTAGAGAGGGCTGAAGGGAAAGAGAGGGCTGACCAGGGTGG					
PERV-B	2620	2640			2660	
					
PERV-A	1990	2000	2010	2020	2030	2040
	TTTGAAGGATGGTTAACAGGTCTCCTGGATGACCACCTGCTTCTGCTCTGACGGGG					
PERV-B	2680	2700			2720	
A					
PERV-A	2050	2060	2070	2080	2090	2100
	CCCCTAGTAGTCCTGCTCCTGTTACTTACAGTTGGCCCTGCTTAATTAGGTTGTT					
PERV-B	2740	2760			2780	
					
PERV-A	2110	2120	2130	2140	2150	2160
	GCCTTGTAGAGAACGAGTGAGTGCAGTCAGATCATGGTACTTAGGCAACAGTACCAA					
PERV-B	2800	2820			2840	
					
PERV-A	2170	2180	2190	2200	2210	2220
	GGCCTCTGAGCCAAGGAGAAACTGACCTCTAGCCTCCCAGTTCTAAGATTAGAACTAT					
PERV-B	2860	2880			2900	
					

Fig. 1e

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PERV-A	2230	2240	2250	2260	2270	2280
	TAACAAGACAAGAAGTGGGAATGAAAGGATGAAAATGCAACCTAACCTCCCAGAACCC					
PERV-B	2920		2940		2960	
					
PERV-A	2290	2300	2310	2320	2330	2340
	AGGAAGTTAATAAAAAGCTCTAAATGCCCGAATTCCAGACCCCTGCTGGCTGCCAGTAA					
PERV-B	2980		3000		3020	
					
PERV-A	2350	2360	2370	2380	2390	2400
	ATAGGTAGAAGGTCACACTCCTATTGTTCCAGGGCCTGCTATCCTGGCTAAGTAAGAT					
PERV-B	3040		3060		3080	
					
PERV-A	2410	2420	2430	2440	2450	2460
	AACAGGAAATGAGTTGACTAATCGCTTATCTGGATTCTGTAAAACCGACTGGCACCATAG					
PERV-B	3100		3120		3140	
					

Fig. 1f

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(71) Applicant (for all designated States except US): MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London WIN 4AL (GB).			
(72) Inventors; and			
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(74) Agents: BRASNETT, Adrian, H. et al.; Mewburn Ellis, York House, 23 Kingsway, London WC2B 6HP (GB).			

(54) Title: **DETECTION OF RETROVIRAL SUBTYPES BASED UPON ENVELOPE SPECIFIC SEQUENCES**

(57) Abstract

The present invention is based upon the finding that porcine endogenous retroviruses exist in two different subtypes, which we have termed PERV-A and PERV-B. The differences are reflected in sequence divergence in the envelope genes, and these differences may be used to provide nucleic acid and antibody probes which can distinguish between the two subtypes. This allows patterns of subtype transmission between cells, particularly porcine to human cells, to be monitored.

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INTERNATIONAL SEARCH REPORT

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A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12Q1/70 C07K16/10 G01N33/569 //C07K14/15,C12N15/48

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B. FIELDS SEARCHED

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Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
T	LE TISSIER ET AL: "Two sets of human-tropic pig virus" NATURE, vol. 389, October 1998, pages 681-82, XP002084123 see the whole document ---	1-18
P, A	WO 97 40167 A (Q ONE BIOTECH LTD :IMUTRAN LTD (GB); GALBRAITH DANIEL NORMAN (GB);) 30 October 1997 see the whole document ---	1-18
P, A	WO 97 21836 A (GEN HOSPITAL CORP) 19 June 1997 see the whole document ---	1-18

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A	<p>PATIENCE C ET AL: "INFECTION OF HUMAN CELLS BY AN ENDOGENOUS RETROVIRUS OF PIGS" NATURE MEDICINE, vol. 3, no. 3, March 1997, pages 282-286, XP002037074 see the whole document</p> <p>---</p>	1-18
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